CLAIMS

What is claimed is:

1. An isolated nucleic acid molecule selected from the group consisting of:

a) a nucleic acid molecule having a nucleotide sequence which is at least 90% identical to the nucleotide sequence of any of SEQ ID NOs: 45, 46, the nucleotide sequence of a cDNA of a clone deposited as ATCC® 207220, or a complement thereof;

b) a nucleic acid molecule comprising at least 100 nucleotide residues and having a nucleotide sequence identical to at least 100 consecutive nucleotide residues of any of SEQ ID NOs: 45, 46, and the nucleotide sequence of a cDNA of a clone deposited as ATCC® 207220, or a complement thereof;

c) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of any of SEQ ID NOs: 47-52, and the amino acid sequence encoded by a cDNA of a clone deposited as ATCC® 207220, or a complement thereof;

d) a nucleic acid molecule which encodes a fragment of a polypeptide comprising the amino acid sequence of any of SEQ ID NOs: 47-52 or the amino acid sequence encoded by a cDNA of a clone deposited as ATCC® 207220, wherein the fragment comprises at least 25 consecutive amino acid residues of any of SEQ ID NOs: 47-52 or the amino acid sequence encoded by a cDNA of a clone deposited as ATCC® 207220; and

e) a nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of any of SEQ ID NOs: 47-52, wherein the nucleic acid molecule hybridizes with a nucleic acid molecule consisting of the nucleotide sequence of any of SEQ ID NOs: 45, 46, and the nucleotide sequence of a cDNA of a clone deposited as ATCC® 207220, or a complement thereof under stringent conditions.

2. The isolated nucleic acid molecule of claim 1, which is selected from the group consisting of:

a) a nucleic acid having the nucleotide sequence of any of SEQ ID NOs: 45, 46, and the nucleotide sequence of a cDNA of a clone deposited as ATCC® 207220, or a complement thereof; and

b) a nucleic acid molecule which encodes a polypeptide having the amino acid sequence of any of SEQ ID NOs: 47-52 or the amino acid sequence encoded by a cDNA of a clone deposited as ATCC® 207220, or a complement thereof.

3. The nucleic acid molecule of claim 1, further comprising vector nucleic acid sequences.

4. The nucleic acid molecule of claim 1 further comprising nucleic acid sequences encoding a heterologous polypeptide.

5. A host cell which contains the nucleic acid molecule of claim 1.

6. The host cell of claim 5 which is a mammalian host cell.

7. A non-human mammalian host cell containing the nucleic acid molecule of claim 1.

8. An isolated polypeptide selected from the group consisting of:

a) a fragment of a polypeptide comprising the amino acid sequence of any of SEQ ID NOs: 47-52 or the amino acid sequence encoded by a cDNA of a clone deposited as ATCC® 207220, wherein the fragment comprises at least 25 contiguous amino acids of any of SEQ ID

NOs: 47-52 or the amino acid sequence encoded by a cDNA of a clone deposited as ATCC® 207220;

b) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of any of SEQ ID NOs: 47-52 or the amino acid sequence encoded by a cDNA of a clone deposited as ATCC® 207220, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule consisting of the nucleotide sequence of any of SEQ ID NOs: 45, 46, and the nucleotide sequence of a cDNA of a clone deposited as ATCC® 207220, or a complement thereof under stringent conditions; and

c) a polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 90% identical to a nucleic acid consisting of the nucleotide sequence of any of SEQ ID NOs: 45, 46, and the nucleotide sequence of a cDNA of a clone deposited as ATCC® 207220, or a complement thereof.

9. The isolated polypeptide of claim 8 having the amino acid sequence of any of SEQ ID NOs: 47-52 or the amino acid sequence encoded by a cDNA of a clone deposited as ATCC® 207220, or a complement thereof.

10. The polypeptide of claim 8, wherein the amino acid sequence of the polypeptide further comprises heterologous amino acid residues.

11. An antibody which selectively binds with the polypeptide of claim 8.

12. A method for producing a polypeptide selected from the group consisting of:

a) a polypeptide having an amino acid sequence comprising any of SEQ ID NOs: 47-52 or the amino acid sequence encoded by a cDNA of a clone deposited as ATCC® 207220, or a complement thereof;

b) a polypeptide comprising a fragment of a protein having the amino acid sequence of any of SEQ ID NOs: 47-52 or the amino acid sequence encoded by a cDNA of a clone deposited as ATCC® 207220, or a complement thereof, wherein the fragment comprises at least 25 contiguous amino acid residues of any of SEQ ID NOs: 47-52 or the amino acid sequence encoded by a cDNA of a clone deposited as ATCC® 207220, or a complement thereof; and

c) a naturally occurring allelic variant of a polypeptide having an amino acid sequence comprising the sequence of any of SEQ ID NOs: 47-52 or the amino acid sequence encoded by a cDNA of a clone deposited as ATCC® 207220, or a complement thereof, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes with a nucleic acid molecule consisting of the nucleotide sequence of any of SEQ ID NOs: 45, 46, and the nucleotide sequence of a cDNA of a clone deposited as ATCC® 207220, or a complement thereof under stringent conditions,

the method comprising culturing the host cell of claim 5 under conditions in which the nucleic acid molecule is expressed.

13. A method for detecting the presence of a polypeptide of claim 8 in a sample, comprising:

a) contacting the sample with a compound which selectively binds with a polypeptide of claim 8; and

b) determining whether the compound binds with the polypeptide in the sample.

14. The method of claim 13, wherein the compound which binds with the polypeptide is an antibody.

15. A kit comprising a compound which selectively binds with a polypeptide of claim 8 and instructions for use.

16. A method for detecting the presence of a nucleic acid molecule of claim 1 in a sample, comprising the steps of:

a) contacting the sample with a nucleic acid probe or primer which selectively hybridizes with the nucleic acid molecule; and

b) determining whether the nucleic acid probe or primer binds with a nucleic acid molecule in the sample.

17. The method of claim 16, wherein the sample comprises mRNA molecules and is contacted with a nucleic acid probe.

18. A kit comprising a compound which selectively hybridizes with a nucleic acid molecule of claim 1 and instructions for use.

19. A method for identifying a compound which binds with a polypeptide of claim 8, the method comprising the steps of:

a) contacting a polypeptide, or a cell expressing a polypeptide of claim 8 with a test compound; and

b) determining whether the polypeptide binds with the test compound.

20. The method of claim 19, wherein the binding of the test compound with the polypeptide is detected by a method selected from the group consisting of:

a) detection of binding by direct detecting of test compound/polypeptide binding;

b) detection of binding using a competition binding assay; and

c) detection of binding using an assay for an activity characteristic of the polypeptide.

21. A method for modulating the activity of a polypeptide of claim 8 comprising contacting the polypeptide or a cell expressing the polypeptide with a compound which binds with the polypeptide in a sufficient concentration to modulate the activity of the polypeptide.

22. A method for identifying a compound which modulates the activity of a polypeptide of claim 8, comprising:

a) contacting the polypeptide with a test compound; and

b) determining the effect of the test compound on the activity of the polypeptide to thereby identify a compound which modulates the activity of the polypeptide.

23. An antibody substance which selectively binds to the polypeptide of claim 8, wherein the antibody substance is made by providing the polypeptide to an immunocompetent vertebrate and thereafter harvesting blood or serum from the vertebrate.

24. A method of assessing whether a first human patient is afflicted with an epithelial or endothelial tumor, the method comprising comparing:

a) occurrence of a nucleic acid molecule of claim 1 in a sample obtained from the first patient and

b) occurrence of the nucleic acid molecule in a control sample selected from the group consisting of

i) a control sample obtained from a tissue that is obtained from the first patient and that is known not to comprise the tumor; and

ii) a control sample obtained from a second patient who is known not to be afflicted with the tumor,

whereby a difference between the first sample and the control sample is an indication that the patient is afflicted with the tumor.

25. The method of claim 24, wherein the tumor is selected from the group consisting of a colon tumor, a prostate tumor, a lung tumor, a pancreatic tumor, and a breast tumor.

26. The method of claim 25, wherein the tumor is a colon tumor.

27. A method of assessing whether a first human patient is afflicted with an epithelial or endothelial tumor, the method comprising comparing

a) occurrence of a nucleic acid molecule of claim 1 in a sample obtained from the first patient and

b) occurrence of the nucleic acid molecule in a control sample selected from the group consisting of

i) a control sample obtained from a tissue that is obtained from the first patient and that is known to comprise the tumor; and

ii) a control sample obtained from a second patient who is known to be afflicted with the tumor,

whereby a difference between the first sample and the control sample is an indication that the patient is not afflicted with the tumor.

28. A method of screening for agents which decrease the activity of a TANGO-294-like lipase protein, the method comprising:

contacting a test compound with a TANGO 294-like lipase polypeptide encoded by an isolated nucleic acid molecule of claim 1 and

detecting binding between the test compound and the TANGO 294-like lipase polypeptide,

wherein binding between the test compound and the TANGO 294-like lipase polypeptide is an indication that the test compound is an agent which decreases the activity of the TANGO 294-like lipase protein.

29. A method of screening for agents which modulate the activity of a TANGO 294-like lipase protein, the method comprising:

contacting a test compound with a TANGO 294-like lipase polypeptide encoded by an isolated nucleic acid molecule of claim 1 and

detecting a TANGO 294-like lipase activity of the polypeptide,

wherein increased TANGO 294-like lipase activity in the presence of the test compound is an indication that the test compound is an agent useful for increasing the activity of the TANGO 294-like lipase protein, and decreased TANGO 294-like lipase activity in the presence of the test compound is an indication that the test compound is an agent useful for decreasing the activity of the TANGO 294-like lipase protein.

30. A method of screening for agents which decrease the activity of a TANGO 294-like lipase protein, the method comprising:

contacting a test compound with an isolated nucleic acid molecule of claim 1 and

detecting binding of the test compound with the isolated nucleic acid molecule,

wherein binding between the test compound and the isolated nucleic acid molecule is an indication that the test compound is a agent useful for decreasing the activity of the TANGO 294-like lipase protein.

31. A method of reducing the activity of a TANGO 294-like lipase protein of a cell, the method comprising contacting the cell with a reagent which specifically binds with an isolated nucleic acid molecule of claim 1, whereby the activity of the TANGO 294-like lipase protein is reduced.

32. A method of reducing the activity of a TANGO 294-like lipase protein of a cell, the method comprising contacting the cell with a reagent which specifically binds with an isolated polypeptide of claim 8, whereby the activity of the TANGO 294-like lipase protein is reduced.

33. A method of making a pharmaceutical composition, the method comprising identifying an agent according to the method of claim 28 and combining the agent and a pharmaceutically acceptable carrier to form the pharmaceutical composition.

34. A method of modulating the activity of a TANGO 294-like lipase protein in a TANGO 294-related disorder, the method comprising making the pharmaceutical composition according to claim 33 and administering the pharmaceutical composition to a human afflicted with the disorder.

35. The method of claim 34, wherein the disorder is selected from the group consisting of a tumor, a disorder of fat absorption, a disorder of fat metabolism, a blood flow disorder, a blood pressure disorder, an inflammatory disorder, an immune disorder, a thrombotic disorder, and a disorder involving inappropriate platelet adherence.

36. The method of claim 35, wherein the disorder is a tumor of endothelial or epithelial origin.

37. The method of claim 35, wherein the disorder is a colon tumor.

38. The method of claim 35, wherein the disorder is a pancreatic tumor.

39. The method of claim 35, wherein the disorder is selected from the group consisting of inadequate expression of gastric lipase, inadequate expression of pancreatic lipase, cystic fibrosis, exocrine pancreatic insufficiency, and obesity.

40. The method of claim 35, wherein the disorder is selected from the group consisting of arterial hypertension, renovascular hypertension, syncope, orthostatic hypotension, and shock.

41. The method of claim 35, wherein the disorder is an inflammatory disorder selected from the group consisting of gastritis, gastric ulcer, colitis, irritable bowel syndrome, inflammatory bowel syndrome, dermatitis, and pancreatitis.

42. The method of claim 35, wherein the disorder is an autoimmune disorder selected from the group consisting of rheumatoid arthritis, psoriasis, myasthenia gravis, an allergy, insulin resistance, systemic lupus erythematosus, scleroderma, and autoimmune diabetes mellitus.

43. The method of claim 35, wherein the disorder is an infection of a human by an infectious agent.

44. The method of claim 43, wherein the infectious agent is human immunodeficiency virus.

45. The method of claim 35, wherein the disorder is selected from the group consisting of hemophilia, stroke, myocardial infarction, coronary artery disease, and atherosclerosis.

46. A method of making a pharmaceutical composition, the method comprising identifying an agent according to the method of claim 29 and combining the agent and a pharmaceutically acceptable carrier to form the pharmaceutical composition.

47. A method of modulating the activity of a TANGO 294-like lipase protein in a TANGO 294-related disorder, the method comprising making the pharmaceutical composition according to claim 46 and administering the pharmaceutical composition to a human afflicted with the disorder.

48. The method of claim 47, wherein the disorder is selected from the group consisting of a tumor, a disorder of fat absorption, a disorder of fat metabolism, a blood flow disorder, a blood pressure disorder, an inflammatory disorder, an immune disorder, a thrombotic disorder, and a disorder involving inappropriate platelet adherence.

49. A method of making a pharmaceutical composition, the method comprising identifying an agent according to the method of claim 30 and combining the agent and a pharmaceutically acceptable carrier to form the pharmaceutical composition.

50. A method of modulating the activity of a TANGO 294-like lipase protein in a TANGO 294-related disorder, the method comprising making the pharmaceutical

composition according to claim 49 and administering the pharmaceutical composition to a human afflicted with the disorder.

51. The method of claim 50, wherein the disorder is selected from the group consisting of a tumor, a disorder of fat absorption, a disorder of fat metabolism, a blood flow disorder, a blood pressure disorder, an inflammatory disorder, an immune disorder, a thrombotic disorder, and a disorder involving inappropriate platelet adherence.